

aaa cag agt cat gca aag agt cta gag tgg att gga ctt att agt act	343
Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile Gly Leu Ile Ser Thr	
95 100	
85	
tac tat ggt gat cct agt tac aac cag agg ttc aag ggc aac aca	391
Tyr Tyr Gly Asp Pro Ser Tyr Asn Gln Arg Phe Lys Gly Lys Ala Thr	
110 115	
105	
atg act gta gac aaa tcc tcc aac aca gcc tat ttg gaa ctt gcc aca	439
Met Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr Leu Glu Leu Ala Arg	
125 130	
120	
ctg aca tct gag gat tct gcc att tat tat tgt gca aga tcg gat ggt	487
Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala Arg Ser Asp Gly	
140 145	
135	
aat tac ggg tat tac tat gct ttg gac tac tgg ggc caa ggc act acg	535
Asn Tyr Gly Tyr Tyr Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr	
155 160	
150	
gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc	583
Val Thr Val Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly	
170 175 180	
165	
ggt ggc gga tcg gat atc gag ctc act cag tct cca tct ttg gct	631
Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser Ser Leu Ala	
185 190 195	
gtg tct cta ggg cag agg gcc acc ata tcc tgc aga gcc agt gaa agt	679
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser	
200 205 210	
gtt gat agt tat ggc gat agt ttt atg cac tgg tat cag cag aaa cca	727
Val Asp Ser Tyr Gly Asp Ser Phe Met His Trp Tyr Gln Gln Lys Pro	
215 220 225	
gga cag cca ccc aaa ctc ctc atc tat cgt gca tcc aac cta gaa tct	775
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser	
230 235 240	
gga gtc cct gcc agg ttc agt ggc agt ggg tct gag tca gac ttc act	823
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Asp Phe Thr	
245 250 260	
ctc acc atc gat cct gtg gag gaa gat gat gct gca gtg tat tac tgt	871
Leu Thr Ile Asp Pro Val Glu Asp Asp Ala Ala Val Tyr Tyr Cys	
265 270 275	
ctg caa agt atg gaa gat ccg tac acg ttc gga ggg acc aag ctg	919
Leu Gln Ser Met Glu Asp Pro Tyr Thr Phe Gly Gly Thr Lys Leu	
280 285 290	
gaa ata aaa cgg gcg gcc gca tcg ggc tcc ggg ggc ggt ggt tct ggt	967
Glu Ile Lys Arg Ala Ala Ser Gly Ser Gly Gly Ser Gly	
295 300 305	

ggt ggt tct ggt ggt ggt tct ggt ggt ggt tct ggt ggt ggt tct ggc gcc agc Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ala Ser 310 315 320	1015
cca gtc cag ttt atc Pro Val Gln Phe Ile 325	1030
<210> 2	
<211> 927	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> scFv encoding sequence	
<221> CDS	
<222> (1)...(927)	
<400> 2	
atg gac tgt ctc acc aac ctc cga tcc gct gag ggt aaa gtt gac cag Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln 1 5 10 15	48
gcg agc aaa atc cta att ctc ctt gtg gct tgg tgg ggg ttt ggg acc Ala Ser Lys Ile Leu Ile Leu Val Ala Trp Trp Gly Phe Gly Thr 20 25 30	96
act gcc gaa gtt tcg act gcc cga gcg gcc cag ccg gcc atg gcc gag Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu 35 40 45	144
gtc aag ctg cag gag tca ggg act gaa ctt gtg aag cct ggg gct tca Val Lys Leu Gln Glu Ser Gly Thr Glu Leu Val Lys Pro Gly Ala Ser 50 55 60	192
gtg aat ctg tct tgc aag gct tct ggc tac acc ttc acc agc tac tgg Val Asn Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp 65 70 75 80	240
atg cac tgg ttg aag cag agg cct gga caa ggc ctt gag tgg atc gga Met His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly 85 90 95	288
gag att gat cct gtt gat agt tat act aac tac aat caa aac ttc aag Glu Ile Asp Pro Val Asp Ser Tyr Thr Asn Tyr Asn Gln Asn Phe Lys 100 105 110	336
ggc aag gcc aca ctg act gta gac aag tcc tcc acc aca gtc tac atg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Val Tyr Met 115 120 125	384
cac ctc agc agc ctg aca tct gag gac tct gcg gtc tat tac tgt gca His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala 130 135 140	432

aga aag ggc tat gct atg gac tac tgg ggc caa ggg acc aac gtc acc	480
Arg Lys Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Asn Val Thr	
145 150 155 160	
gtc tcc tca ggt gga tgc ggt tca ggc gga ggt ggc tct ggc ggt ggc	528
Val Ser Ser Gly Gly Cys Gly Ser Gly Gly Gly Ser Gly Gly Gly	
165 170 175	
gga tcg gac atc gag ctc act cag tca cca gca atc atg tct gca tct	576
Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser	
180 185 190	
cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca agt ata agt	624
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ile Ser	
195 200 205	
tac atg cac tgg tac cag cag aag cca ggc acc tcc ccc aaa aga tgg	672
Tyr Met His Trp Tyr Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp	
210 215 220	
att tat gac aca tcc aaa ctg gct tct gga gtc cct gct cgc ttc agt	720
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser	
225 230 235 240	
ggc agt ggg tct ggg acc tct tat tct ctc cca atc agc agc atg gag	768
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Pro Ile Ser Ser Met Glu	
245 250 255	
gct gaa gat gct gcc act tat tac tgc cat cag cgg agt agt tac cca	816
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro	
260 265 270	
tgg acg ttc ggt gga ggg acc aag ctg gaa ata aaa cgg gcg gcc gca	864
Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala	
275 280 285	
tcg ggc tcc ggg ggc ggt ggt tct ggt ggt tct ggt ggt ggt ggt	912
Ser Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Gly Gly	
290 295 300	
tct ggt ggt ggt ggt	927
Ser Gly Gly Gly	
305	

<210> 3
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> scFv encoding sequence

<221> CDS
<222> (1)...(990)

<400> 3 atg gac tgt ctc acc aac ctc cga tcc gct gag ggt aaa gtt gac cag Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln 5 10 15	48
gct agc aaa atc cta att ctc ctt gtg gct tgg tgg ttt ggg acc Ala Ser Lys Ile Leu Ile Leu Val Ala Trp Trp Gly Phe Gly Thr 20 25 30	96
act gcc gaa gtt tcg act gcc cga gct ccc cag gcc atg gcc cag Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Gln 40 45	144
gtg cag ctg cag cag tct ggg act gaa ctg gca aca cct ggg gcc tca Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Ala Thr Pro Gly Ala Ser 50 55 60	192
gtg agg atg tcc tgc aag gct tct ggc tac gcc ttt act acc tac tgg Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Tyr Trp 70 75 80	240
atg cac tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly 85 90 95	288
tac att aat cct acc act gat tat act gac tac aat ctg aag ttc aag Tyr Ile Asn Pro Thr Thr Asp Tyr Thr Asp Tyr Asn Leu Lys Phe Lys 100 105 110	336
gac aag gcc aca ttg act gca gac aaa tcc tcc agt aca gcc tac atg Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met 115 120 125	384
caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala 130 135 140	432
aga tcg ggg tgg tcc tat gct atg gac tac tgg ggg caa ggg acc acg Arg Ser Gly Trp Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr 145 150 155 160	480
gtc acc atc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc Val Thr Ile Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly 165 170 175	528
ggt ggc gga tcg gac atc gag ctc act cag tct cca gca atc atg tct Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser 180 185 190	576
gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser 195 200 205	624
gta agt tac atg cac tgg ttc cag cag aag cca ggc act tct ccc aaa Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys 210 215 220	672

ctc tgg att tat agc aca tcc aac ctc gct tct gga gtc cct gct cgc	720
Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg	
225 230 235 240	
ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga	768
Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg	
245 250 255	
atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg agt agt	816
Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser	
260 265 270	
tac cca ttc acg ttc ggc tcg ggc acc aag ctg gaa atc aaa cgg gcg	864
Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala	
275 280 285	
gcc gca tcg ggc tcc ggg ggc ggt ggt tct ggt ggt ggt tct ggt	912
Ala Ala Ser Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly	
290 295 300	
ggt ggt ggt tct ggt ggt tct ggc gcc agc cca gtc cag ttt	960
Gly Gly Gly Ser Gly Gly Ser Gly Ala Ser Pro Val Gln Phe	
305 310 315 320	
atc ccc ctg ctt gtg ggt cta ggg att tca	990
Ile Pro Leu Leu Val Gly Leu Gly Ile Ser	
325 330	
<210> 4	
<211> 946	
<212> DNA	
<213> Artificial Sequence	
<220>	
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<221> CDS	
<222> (1)...(945)	
<400> 4	
atg gac tgt ctc acc aac ctc cga tcc gct gag ggt aaa gtt gac cag	48
Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln	
1 5 10 15	
gcg agc aaa atc cta att ctc ctt gtg gct tgg tgg ggg ttt ggg acc	96
Ala Ser Lys Ile Leu Ile Leu Val Ala Trp Trp Gly Phe Gly Thr	
20 25 30	
act gcc gaa gtt tcg act gcc cga gcg gcc cag ccg gcc atg gcc gag	144
Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu	
35 40 45	
gtc aag ctg cag cag tca ggg gct gag ctg gtg agg cct gga gct tca	192
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser	
50 55 60	

gtg aag ctg tcc tgc aag act tct ggc ttc tcc ttc acc agc tac tgg Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Ser Phe Thr Ser Tyr Trp 65 70 75 80	240
atg aac tgg gtg aag ctg agg cct gga caa ggc ctt gag tgg att ggc Met Asn Trp Val Lys Leu Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly 85 90 95	288
atg att cat cct tcc gat agt gaa act agt tta act cag agg ttc aag Met Ile His Pro Ser Asp Ser Glu Thr Ser Leu Thr Gln Arg Phe Lys 100 105 110	336
gac aag gcc aca ctg act gta gac aaa tcc tcc agc aca gcc tac atg Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr Met 115 120 125	384
caa ctc agc agc ccg aca tct gag gac tct gcg gtc tat tac tgt gca Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala 130 135 140	432
aga tct ctt tat gct aac tac ccc tcc tgg ttt act tac tgg ggc caa Arg Ser Leu Tyr Ala Asn Tyr Pro Ser Trp Phe Thr Tyr Trp Gly Gln 145 150 155 160	480
ggc acc acg gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly 165 170 175	528
ggc tct ggc ggt ggc gga tcg gac atc gag ctc act cag tct cca acc Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr 180 185 190	576
acc atg gct gca tct ccc ggg gag aag atc act atc acc tgc agt gcc Thr Met Ala Ala Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala 195 200 205	624
agc tca agt ata agt tcc aat tac ttg cat tgg tat cag cag aag cca Ser Ser Ser Ile Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro 210 215 220	672
gga ttc tcc cct aaa ctc ttg att tat agg aca tcc aat ctg gct tct Gly Phe Ser Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser 225 230 235 240	720
gga gtc cca gct cgc ttc agt ggc agt ggg tct ggg acc tct tac tct Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser 245 250 255	768
ctc aca att ggc acc atg gag gct gaa gat gtt gcc act tac tac tgc Leu Thr Ile Gly Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys 260 265 270	816
cag cag ggt agt agt ata ccg tac acg ttc gga ggg acc aag ctg Gln Gln Gly Ser Ser Ile Pro Tyr Thr Phe Gly Gly Thr Lys Leu 275 280 285	864

gaa ata aaa cgg gcg gcc gca tcg ggc tcc ggg ggc ggt tct ggt 912
 Glu Ile Lys Arg Ala Ala Ser Gly Ser Gly Gly Gly Ser Gly
 295 300
 290 946
 ggt ggt ggt tct ggt ggt tct ggt ggt g 305
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly 310 315
 305
 <210> 5
 <211> 906
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> scFv encoding sequence
 <221> CDS
 <222> (1)...(906)
 <400> 5 48
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 Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 5 10 15
 1
 gcg agc aaa atc cta att ctc ctt gtg gct tgg tgg ggg ttt ggg acc 96
 Ala Ser Lys Ile Leu Ile Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30
 act gcc gaa gtt tcg act gcc cga gcg gcc cag ccg gcc atg gcc cag 144
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Gln
 35 40 45
 gta cag ctg cag cag tca gga gca gaa atg aaa aag ccc ggg gag tct 192
 Val Gln Leu Gln Gln Ser Gly Ala Glu Met Lys Lys Pro Gly Glu Ser
 50 55 60
 ctg aaa atc tcc tgt aag ggt ttt gga tac ttt agc acc tac tgg 240
 Leu Lys Ile Ser Cys Lys Gly Phe Gly Tyr Asp Phe Ser Thr Tyr Trp
 65 70 75 80
 atc gcc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag tac atg ggg 288
 Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met Gly
 85 90 95
 ctc atc tat cct ggt gac tct gac acc aaa tac agc ccg tcc ttc caa 336
 Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe Gln
 100 105 110
 ggc cag gtc acc atc tca gcc gac aag tcc atc agc acc gcc tac ctg 384
 Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
 115 120 125
 cag tgg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt gcg 432
 Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
 130 135 140

aga gtc tct gga tat tgt agt agt acc acc tgc tat gac tac tac tac	480
Arg Val Ser Gly Tyr Cys Ser Ser Thr Ser Cys Tyr Asp Tyr Tyr Tyr	
145 150 155 160	
tac tac atg gac gtc tgg ggc cgg gga acc ctg gtc acc gtc tcg aga	528
Tyr Tyr Met Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Arg	
165 170 175	
ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac	576
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Asp	
180 185 190	
atc gtg atg acc cag tct cct tcc acc ctg tct gca tct gta gga gac	624
Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp	
195 200 205	
aga gtc acc atg act tgc cgg gcc agt cag aac att aat atc tgg ttg	672
Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asn Ile Asn Ile Trp Leu	
210 215 220	
gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat	720
Ala Trp Tyr Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr	
225 230 235 240	
aag gcg tcc act tta gag agt ggg gtc ccc tca agg ttc agc ggc agt	768
Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser	
245 250 255	
gga tct ggg aca gaa ttc act ctc acc atc agc ggc ctg cag cct gat	816
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro Asp	
260 265 270	
gat ttt gca agt tat tac tgt caa cgg tat gat agt gac tgg tcg ttc	864
Asp Phe Ala Ser Tyr Tyr Cys Gln Arg Tyr Asp Ser Asp Trp Ser Phe	
275 280 285	
ggc caa ggg acc aag ctg gag atc aaa cgt gcg gcc gca tcg	906
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ser	
290 295 300	
<210> 6	
<211> 329	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> scFv	
<400> 6	
Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln	
1 5 10 15	
Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr	
20 25 30	
Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu	
35 40 45	
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Val Ser	
50 55 60	

Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr Gly
 65 70 75 80
 Met Ser Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile Gly
 85 90 95
 Leu Ile Ser Thr Tyr Tyr Gly Asp Pro Ser Tyr Asn Gln Arg Phe Lys
 100 105 110
 Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr Leu
 115 120 125
 Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
 130 135 140
 Arg Ser Asp Gly Asn Tyr Gly Tyr Tyr Ala Leu Asp Tyr Trp Gly
 145 150 155 160
 Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
 165 170 175
 Gly Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro
 180 185 190
 Ser Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg
 195 200 205
 Ala Ser Glu Ser Val Asp Ser Tyr Gly Asp Ser Phe Met His Trp Tyr
 210 215 220
 Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser
 225 230 235 240
 Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Glu
 245 250 255
 Ser Asp Phe Thr Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Ala Ala
 260 265 270
 Val Tyr Tyr Cys Leu Gln Ser Met Glu Asp Pro Tyr Thr Phe Gly Gly
 275 280 285
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ser Gly Ser Gly Gly
 290 295 300
 Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Gly
 305 310 315 320
 Ser Gly Ala Ser Pro Val Gln Phe Ile
 325

<210> 7
 <211> 309
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<400> 7
 Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 1 5 10 15
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu
 35 40 45
 Val Lys Leu Gln Glu Ser Gly Thr Glu Leu Val Lys Pro Gly Ala Ser
 50 55 60
 Val Asn Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp
 65 70 75 80
 Met His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
 85 90 95

Glu Ile Asp Pro Val Asp Ser Tyr Thr Asn Tyr Asn Gln Asn Phe Lys
 100 105 110
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Val Tyr Met
 115 120 125
 His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 130 135 140
 Arg Lys Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Asn Val Thr
 145 150 155 160
 Val Ser Ser Gly Gly Cys Gly Ser Gly Gly Gly Ser Gly Gly Gly
 165 170 175
 Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
 180 185 190
 Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ile Ser
 195 200 205
 Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp
 210 215 220
 Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
 225 230 235 240
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Pro Ile Ser Ser Met Glu
 245 250 255
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro
 260 265 270
 Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala
 275 280 285
 Ser Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
 290 295 300
 Ser Gly Gly Gly Gly
 305

<210> 8
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<400> 8

Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 1 5 10 15
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Gln
 35 40 45
 Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Ala Thr Pro Gly Ala Ser
 50 55 60
 Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Tyr Trp
 65 70 75 80
 Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
 85 90 95
 Tyr Ile Asn Pro Thr Thr Asp Tyr Thr Asp Tyr Asn Leu Lys Phe Lys
 100 105 110
 Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
 115 120 125
 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 130 135 140

Arg Ser Gly Trp Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 145 150 155 160
 Val Thr Ile Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
 165 170 175
 Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser
 180 185 190
 Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser
 195 200 205
 Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys
 210 215 220
 Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
 225 230 235 240
 Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg
 245 250 255
 Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser
 260 265 270
 Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala
 275 280 285
 Ala Ala Ser Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly
 290 295 300
 Gly Gly Gly Ser Gly Gly Ser Gly Ala Ser Pro Val Gln Phe
 305 310 315 320
 Ile Pro Leu Leu Val Gly Leu Gly Ile Ser
 325 330

<210> 9
 <211> 315
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<400> 9
 Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 1 5 10 15
 Ala Ser Lys Ile Leu Ile Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu
 35 40 45
 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser
 50 55 60
 Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Ser Phe Thr Ser Tyr Trp
 65 70 75 80
 Met Asn Trp Val Lys Leu Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
 85 90 95
 Met Ile His Pro Ser Asp Ser Glu Thr Ser Leu Thr Gln Arg Phe Lys
 100 105 110
 Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
 115 120 125
 Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 130 135 140
 Arg Ser Leu Tyr Ala Asn Tyr Pro Ser Trp Phe Thr Tyr Trp Gly Gln
 145 150 155 160
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 165 170 175

Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr
 180 185 190
 Thr Met Ala Ala Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala
 195 200 205
 Ser Ser Ser Ile Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro
 210 215 220
 Gly Phe Ser Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser
 225 230 235 240
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
 245 250 255
 Leu Thr Ile Gly Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys
 260 265 270
 Gln Gln Gly Ser Ser Ile Pro Tyr Thr Phe Gly Gly Thr Lys Leu
 275 280 285
 Glu Ile Lys Arg Ala Ala Ala Ser Gly Ser Gly Gly Ser Gly
 290 295 300
 Gly Gly Gly Ser Gly Gly Ser Gly Gly
 305 310 315

<210> 10

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 10

Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 1 5 10 15
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Gln
 35 40 45
 Val Gln Leu Gln Gln Ser Gly Ala Glu Met Lys Lys Pro Gly Glu Ser
 50 55 60
 Leu Lys Ile Ser Cys Lys Gly Phe Gly Tyr Asp Phe Ser Thr Tyr Trp
 65 70 75 80
 Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met Gly
 85 90 95
 Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe Gln
 100 105 110
 Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
 115 120 125
 Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
 130 135 140
 Arg Val Ser Gly Tyr Cys Ser Ser Thr Ser Cys Tyr Asp Tyr Tyr Tyr
 145 150 155 160
 Tyr Tyr Met Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Arg
 165 170 175
 Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Asp
 180 185 190
 Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp
 195 200 205
 Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asn Ile Asn Ile Trp Leu
 210 215 220

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
225 230 235 240
Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
245 250 255
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro Asp
260 265 270
Asp Phe Ala Ser Tyr Tyr Cys Gln Arg Tyr Asp Ser Asp Trp Ser Phe
275 280 285
Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ser
290 295 300